

# SEQUENCE LISTING

<110> Jackson, W. James  
Pace, John

<120> Chlamydia Protein, Gene Sequence and Uses Thereof

<130> 7969-062-999

<140> 08/942,596

<141> 1997-10-02

<160> 43

<170> PatentIn version 3.0

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Recombinant Expression Vector

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aagataagaa cattttattga tattaataatta ttaatttttt atgaagcggg gtaattaatt	360
ttatctctca gcttttgtgt g atg caa acg tct ttc cat aag ttc ttt ctt	411
Met Gln Thr Ser Phe His Lys Phe Phe Leu	
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tca atg att cta gct tat tct tgc tgc tct tta aat ggg ggg gga tat	459
Ser Met Ile Leu Ala Tyr Ser Cys Cys Ser Leu Asn Gly Gly Gly Tyr	
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Ala Ala Glu Ile Met Val Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu	
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Thr Val Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr	
45 50 55	
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Val Phe Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile	
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gca gct ttg cct tta agt tgt ttt ggg aac tta tta ggg agt ttt act	651
Ala Ala Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr	
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ggt tta ggg aga gga cac tcg ttg act ttc gag aac ata cgg act tct	699
Val Leu Gly Arg Gly His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser	
95 100 105	
aca aat ggg gca gct cta agt aat agc gct gct gat gga ctg ttt act	747
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Ile Glu Gly Phe Lys Glu Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu	
125 130 135	
gcc gta ctg cct gct gca acg act aat aag ggt agc cag act ccg acg	843
Ala Val Leu Pro Ala Ala Thr Thr Asn Lys Gly Ser Gln Thr Pro Thr	
140 145 150	
aca aca tct aca ccg tct aat ggt act att tat tct aaa aca gat ctt	891
Thr Thr Ser Thr Pro Ser Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu	
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Leu Leu Leu Asn Asn Glu Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser	
175 180 185	
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Gly Asp Gly Gly Ala Ile Asp Ala Lys Ser Leu Thr Val Gln Gly Ile	
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Ser Lys Leu Cys Val Phe Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly	
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Phe Leu Asn Asn Gly Lys Thr Leu Phe Leu Asn Asn Val Ala Ser Pro	
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Val Tyr Ile Ala Ala Lys Gln Pro Thr Ser Gly Gln Ala Ser Asn Thr	
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Gln Ala Gly Ser Asn Asn Ser Gly Ser Val Ser Phe Asp Gly Glu Gly	
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Val Val Phe Phe Ser Ser Asn Val Ala Ala Gly Lys Gly Gly Ala Ile	
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Tyr Ala Lys Lys Leu Ser Val Ala Asn Cys Gly Pro Val Gln Phe Leu	
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Arg Asn Ile Ala Asn Asp Gly Gly Ala Ile Tyr Leu Gly Glu Ser Gly	
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Glu Leu Ser Leu Ser Ala Asp Tyr Gly Asp Ile Ile Phe Asp Gly Asn	
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Met Ala Asn Gly Asn Asn Gln Pro Ala Gln Ser Ser Lys Leu Leu Lys	
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Ile Asn Asp Gly Glu Gly Tyr Thr Gly Asp Ile Val Phe Ala Asn Gly	
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Ser Ser Thr Leu Tyr Gln Asn Val Thr Ile Glu Gln Gly Arg Ile Val	
510 515 520	
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Gly Ser Leu Tyr Met Glu Ala Gly Ser Thr Trp Asp Phe Val Thr Pro	
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Gln Pro Pro Gln Gln Pro Pro Ala Ala Asn Gln Leu Ile Thr Leu Ser	
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Asn Leu His Leu Ser Leu Ser Ser Leu Leu Ala Asn Asn Ala Val Thr	
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aat cct cct acc aat cct cca gcg caa gat tct cat cct gca gtc att	2187
Asn Pro Pro Thr Asn Pro Pro Ala Gln Asp Ser His Pro Ala Val Ile	
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Gly Ser Thr Thr Ala Gly Ser Val Thr Ile Ser Gly Pro Ile Phe Phe	
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Glu Asp Leu Asp Asp Thr Ala Tyr Asp Arg Tyr Asp Trp Leu Gly Ser	
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Ala Asn Ala Pro Ser Asp Leu Thr Leu Gly Asn Glu Met Pro Lys Tyr	
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Gly Tyr Gln Gly Ser Trp Lys Leu Ala Trp Asp Pro Asn Thr Ala Asn	
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Val Cys Arg Ser Asn His His Ala Cys Ile Gly Ser Val Tyr Leu Ser	
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acc caa caa gct tta tgt gga tcc tat ttg ttc gga gat gcg ttt atc	2859
Thr Gln Gln Ala Leu Cys Gly Ser Tyr Leu Phe Gly Asp Ala Phe Ile	
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Arg Ala Ser Tyr Gly Phe Gly Asn Gln His Met Lys Thr Ser Tyr Thr	
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Glu Ile Gly Ala Gly Leu Pro Ile Val Ile Thr Pro Ser Lys Leu Tyr	
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His Glu Ser Phe Thr Glu Glu Gly Asp Gln Ala Arg Ala Phe Lys Ser	
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Gly His Leu Leu Asn Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg	
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tgt tct agt aca cat cct aat aaa tat agc ttt atg gcg gct tat atc	3195
Cys Ser Ser Thr His Pro Asn Lys Tyr Ser Phe Met Ala Ala Tyr Ile	
925 930 935	
tgt gat gct tat cgc acc atc tct ggt act gag aca acg ctc cta tcc	3243
Cys Asp Ala Tyr Arg Thr Ile Ser Gly Thr Glu Thr Thr Leu Leu Ser	
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His Gln Glu Thr Trp Thr Thr Asp Ala Phe His Leu Ala Arg His Gly	
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Val Tyr Gly His Gly Arg Tyr Glu Tyr Arg Asp Ala Ser Arg Gly Tyr	
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aatacgagta	ataattacgg	agatggagga	gctatcttct	gtaagaatgg	tgcgcaagca	960
ggatccaata	actctggatc	agtttccctt	gatggagagg	gagtagtttt	ctttagtagc	1020
aatgtagctg	ctgggaaagg	gggagctatt	tatgccaaaa	agctctcggt	tgctaactgt	1080
ggccctgtac	aattttttaag	gaatatcgct	aatgatggtg	gagcgattta	tttaggagaa	1140
tctggagagc	tcagtttatc	tgctgattat	ggagatatta	ttttcgatgg	gaatcttaaa	1200
agaacagcca	aagagaatgc	tgccgaatgt	aatggcgtaa	ctgtgtcctc	acaagccatt	1260
tcgatgggat	cgggagggaa	aataacgaca	ttaagagcta	aagcagggca	tcagattctc	1320
tttaatgatc	ccatcgagat	ggcaaacgga	aataaccagc	cagcgagtc	ttccaaactt	1380
ctaaaaatta	acgatggtga	aggatacaca	ggggatattg	tttttgctaa	tggaagcagt	1440
actttgtacc	aaaatgttac	gatagagcaa	ggaaggattg	ttcttcgtga	aaaggcaaaa	1500
ttatcagtga	a					1511

<210> 11  
 <211> 1444  
 <212> DNA  
 <213> Chlamydia sp.

<400> 11						
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aactccacaa	ccaccacaac	agcctcctgc	cgctaatacag	ttgatcacgc	tttccaatct	120
gcatttgtct	ctttcttctt	tgtagcaaaa	caatgcagtt	acgaatcctc	ctaccaatcc	180
tccagcgcaa	gattctcatc	ctgcagtcac	tgtagcaca	actgctgggt	ctgttacaat	240
tagtgggctt	atcttttttg	aggatttgga	tgatacagct	tatgataggt	atgattggct	300
aggttctaata	caaaaaatca	atgtcctgaa	attacagtta	gggactaagc	ccccagctaa	360
tgccccatca	gatttgactc	tagggaatga	gatgcctaag	tatggctatc	aaggaagctg	420
gaagcttgcg	tgggatoccta	atacagcaaa	taatggctct	tatactctga	aagctacatg	480
gactaaaact	gggtataatc	ctgggcctga	gcgagtagct	tctttgggtc	caaatagttt	540
atggggatcc	attttagata	tacgatctgc	gcattcagca	attcaagcaa	gtgtggatgg	600
gcgctcttat	tgtagaggat	tatgggtttc	tgtagtttcg	aatttcttct	atcatgaccg	660
cgatgcttta	ggtaggggat	atcggtatat	tagtgggggt	tattccttag	gagcaaaactc	720
ctactttgga	tcacatgatg	ttggtctagc	atttaccgaa	gtattttggt	gatctaaaga	780
ttatgtatgt	tgtagttcca	atcatcatgc	ttgcatagga	tccgtttatc	tatctaccca	840
acaagcttta	tgtggatcct	atttgttcgg	agatgcgttt	atccgtgcta	gctacgggtt	900
tgggaatcag	catatgaaaa	cctcatatac	atttgcagag	gagagcgatg	ttcgttggga	960
taataactgt	ctggctggag	agattggagc	gggattaccg	attgtgatta	ctccatctaa	1020
gctctatttg	aatgagttgc	gtcctttcgt	gcaagctgag	ttttcttatg	ccgatcatga	1080
atctttttaca	gaggaaggcg	atcaagctcg	ggcattcaag	agcggacatc	tcctaaatct	1140
atcagttcct	gttggagtga	agtttgatcg	atgttctagt	acacatccta	ataaatatag	1200
cttttagggc	gcttatatct	gtgatgctta	tcgcaccatc	tctggtagctg	agacaacgct	1260
cctatcccat	caagagacat	ggacaacaga	tgcctttcat	ttagcaagac	atggagttgt	1320
ggtagagga	tctatgtatg	cttctctaac	aagtaataata	gaagtatatg	gccatggaag	1380
atatgagtat	cgagatgctt	ctcgaggcta	tggtttgagt	gcaggaagta	gagtcgggtt	1440
ctaa						1444

<210> 12  
 <211> 56  
 <212> DNA  
 <213> Chlamydia sp.

<400> 12	aagggcccaa	ttacgcagag	ggtaccgaaa	ttatggttcc	tcaaggaatt	tacgat	56
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<210> 13  
 <211> 56  
 <212> DNA  
 <213> Chlamydia sp.

<400> 13  
aagggcccaa ttacgcagag ggtaccctaa gaagaaggca tgccgtgcta gcggag 56

<210> 14  
<211> 57  
<212> DNA  
<213> Chlamydia sp.

<400> 14  
aagggcccaa ttacgcagag ggtaccggag agctcgcgaa tccatacgaa taggaac 57

<210> 15  
<211> 1013  
<212> PRT  
<213> Chlamydia sp.

<400> 15  
Met Gln Thr Ser Phe His Lys Phe Phe Leu Ser Met Ile Leu Ala Tyr  
1 5 10 15  
Ser Cys Cys Ser Leu Asn Gly Gly Gly Tyr Ala Ala Glu Ile Met Val  
20 25 30  
Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu Thr Val Ser Phe Pro Tyr  
35 40 45  
Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe Ser Ala Gly Glu  
50 55 60  
Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala Leu Pro Leu Ser  
65 70 75 80  
Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu Gly Arg Gly His  
85 90 95  
Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn Gly Ala Ala Leu  
100 105 110  
Ser Asp Ser Ala Asn Ser Gly Leu Phe Thr Ile Glu Gly Phe Lys Glu  
115 120 125  
Leu Ser Phe Ser Asn Cys Asn Pro Leu Leu Ala Val Leu Pro Ala Ala  
130 135 140  
Thr Thr Asn Asn Gly Ser Gln Thr Pro Ser Thr Thr Ser Thr Pro Ser  
145 150 155 160  
Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu Leu Asn Asn Glu  
165 170 175  
Lys Phe Ser Phe Tyr Ser Asn Ser Val Ser Gly Asp Gly Gly Ala Ile  
180 185 190  
Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys Leu Cys Val Phe  
195 200 205  
Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys Gln Val Val Thr  
210 215 220  
Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala Phe Val Ala Asn  
225 230 235 240  
Val Ala Gly Val Arg Gly Gly Gly Ile Ala Ala Val Gln Asp Gly Gln  
245 250 255  
Gln Gly Val Ser Ser Ser Thr Ser Thr Glu Asp Pro Val Val Ser Phe  
260 265 270  
Ser Arg Asn Thr Ala Val Glu Phe Asp Gly Asn Val Ala Arg Val Gly  
275 280 285  
Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu Asn Asn Gly Lys  
290 295 300  
Thr Leu Phe Leu Asn Asn Val Ala Ser Pro Val Tyr Ile Ala Ala Glu  
305 310 315 320  
Gln Pro Thr Asn Gly Gln Ala Ser Asn Thr Ser Asp Asn Tyr Gly Asp  
325 330 335  
Gly Gly Ala Ile Phe Cys Lys Asn Gly Ala Gln Ala Ala Gly Ser Asn  
340 345 350

Asn	Ser	Gly	Ser	Val	Ser	Phe	Asp	Gly	Glu	Gly	Val	Val	Phe	Phe	Ser
		355					360					365			
Ser	Asn	Val	Ala	Ala	Gly	Lys	Gly	Gly	Ala	Ile	Tyr	Ala	Lys	Lys	Leu
		370				375					380				
Ser	Val	Ala	Asn	Cys	Gly	Pro	Val	Gln	Leu	Leu	Gly	Asn	Ile	Ala	Asn
385					390					395					400
Asp	Gly	Gly	Ala	Ile	Tyr	Leu	Gly	Glu	Ser	Gly	Glu	Leu	Ser	Leu	Ser
			405					410						415	
Ala	Asp	Tyr	Gly	Asp	Met	Ile	Phe	Asp	Gly	Asn	Leu	Lys	Arg	Thr	Ala
			420					425					430		
Lys	Glu	Asn	Ala	Ala	Asp	Val	Asn	Gly	Val	Thr	Val	Ser	Ser	Gln	Ala
		435					440					445			
Ile	Ser	Met	Gly	Ser	Gly	Gly	Lys	Ile	Thr	Thr	Leu	Arg	Ala	Lys	Ala
		450				455					460				
Gly	His	Gln	Ile	Leu	Phe	Asn	Asp	Pro	Ile	Glu	Met	Ala	Asn	Gly	Asn
465					470					475					480
Asn	Gln	Pro	Ala	Gln	Ser	Ser	Glu	Pro	Leu	Lys	Ile	Asn	Asp	Gly	Glu
				485					490					495	
Gly	Tyr	Thr	Gly	Asp	Ile	Val	Phe	Ala	Asn	Gly	Asn	Ser	Thr	Leu	Tyr
			500					505					510		
Gln	Asn	Val	Thr	Ile	Glu	Gln	Gly	Arg	Ile	Val	Leu	Arg	Glu	Lys	Ala
		515					520					525			
Lys	Leu	Ser	Val	Asn	Ser	Leu	Ser	Gln	Thr	Gly	Gly	Ser	Leu	Tyr	Met
		530				535					540				
Glu	Ala	Gly	Ser	Thr	Leu	Asp	Phe	Val	Thr	Pro	Gln	Pro	Pro	Gln	Gln
545					550					555					560
Pro	Pro	Ala	Ala	Asn	Gln	Ser	Ile	Thr	Leu	Ser	Asn	Leu	His	Leu	Ser
				565					570					575	
Leu	Ser	Ser	Leu	Leu	Ala	Asn	Asn	Ala	Val	Thr	Asn	Pro	Pro	Thr	Asn
			580					585					590		
Pro	Pro	Ala	Gln	Asp	Ser	His	Pro	Ala	Val	Ile	Gly	Ser	Thr	Thr	Ala
		595					600					605			
Gly	Ser	Val	Thr	Ile	Ser	Gly	Pro	Ile	Phe	Phe	Glu	Asp	Leu	Asp	Asp
		610				615					620				
Thr	Ala	Tyr	Asp	Arg	Tyr	Asp	Trp	Leu	Gly	Ser	Asn	Gln	Lys	Ile	Asp
625					630					635					640
Val	Leu	Lys	Leu	Gln	Leu	Gly	Thr	Gln	Pro	Pro	Ala	Asn	Ala	Pro	Ser
				645					650					655	
Asp	Leu	Thr	Leu	Gly	Asn	Glu	Met	Pro	Lys	Tyr	Gly	Tyr	Gln	Gly	Ser
			660					665					670		
Trp	Lys	Leu	Ala	Trp	Asp	Pro	Asn	Thr	Ala	Asn	Asn	Gly	Pro	Tyr	Thr
		675					680					685			
Leu	Lys	Ala	Thr	Trp	Thr	Lys	Thr	Gly	Tyr	Asn	Pro	Gly	Pro	Glu	Arg
		690				695					700				
Val	Ala	Ser	Leu	Val	Pro	Asn	Ser	Leu	Trp	Gly	Ser	Ile	Leu	Asp	Ile
705					710					715					720
Arg	Ser	Ala	His	Ser	Ala	Ile	Gln	Ala	Ser	Val	Asp	Gly	Arg	Ser	Tyr
				725					730					735	
Cys	Arg	Gly	Leu	Trp	Val	Ser	Gly	Val	Ser	Asn	Phe	Phe	Tyr	His	Asp
			740					745					750		
Arg	Asp	Ala	Leu	Gly	Gln	Gly	Tyr	Arg	Tyr	Ile	Ser	Gly	Gly	Tyr	Ser
		755					760					765			
Leu	Gly	Ala	Asn	Ser	Tyr	Phe	Gly	Ser	Ser	Met	Phe	Gly	Leu	Ala	Phe
		770				775					780				
Thr	Glu	Val	Phe	Gly	Arg	Ser	Lys	Asp	Tyr	Val	Val	Cys	Arg	Ser	Asn
785					790					795					800
His	His	Ala	Cys	Ile	Gly	Ser	Val	Tyr	Leu	Ser	Thr	Lys	Gln	Ala	Leu
				805					810					815	
Cys	Gly	Ser	Tyr	Val	Phe	Gly	Asp	Ala	Phe	Ile	Arg	Ala	Ser	Tyr	Gly
			820					825					830		
Phe	Gly	Asn	Gln	His	Met	Lys	Thr	Ser	Tyr	Thr	Phe	Ala	Glu	Glu	Ser
		835					840					845			

Asp Val Cys Trp Asp Asn Asn Cys Leu Val Gly Glu Ile Gly Val Gly  
 850 855 860  
 Leu Pro Ile Val Ile Thr Pro Ser Lys Leu Tyr Leu Asn Glu Leu Arg  
 865 870 875 880  
 Pro Phe Val Gln Ala Glu Phe Ser Tyr Ala Asp His Glu Ser Phe Thr  
 885 890 895  
 Glu Glu Gly Asp Gln Ala Arg Ala Phe Arg Ser Gly His Leu Met Asn  
 900 905 910  
 Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg Cys Ser Ser Thr His  
 915 920 925  
 Pro Asn Lys Tyr Ser Phe Met Gly Ala Tyr Ile Cys Asp Ala Tyr Arg  
 930 935 940  
 Thr Ile Ser Gly Thr Gln Thr Thr Leu Leu Ser His Gln Glu Thr Trp  
 945 950 955 960  
 Thr Thr Asp Ala Phe His Leu Ala Arg His Gly Val Ile Val Arg Gly  
 965 970 975  
 Ser Met Tyr Ala Ser Leu Thr Ser Asn Ile Glu Val Tyr Gly His Gly  
 980 985 990  
 Arg Tyr Glu Tyr Arg Asp Thr Ser Arg Gly Tyr Gly Leu Ser Ala Gly  
 995 1000 1005  
 Ser Lys Val Arg Phe  
 1010

<210> 16  
 <211> 1013  
 <212> PRT  
 <213> Chlamydia sp.

<400> 16  
 Met Gln Thr Ser Phe His Lys Phe Phe Leu Ser Met Ile Leu Ala Tyr  
 1 5 10 15  
 Ser Cys Cys Ser Leu Thr Gly Gly Gly Tyr Ala Ala Glu Ile Met Val  
 20 25 30  
 Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu Thr Val Ser Phe Pro Tyr  
 35 40 45  
 Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe Ser Ala Gly Glu  
 50 55 60  
 Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala Leu Pro Leu Ser  
 65 70 75 80  
 Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu Gly Arg Gly His  
 85 90 95  
 Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn Gly Ala Ala Leu  
 100 105 110  
 Ser Asp Ser Ala Asn Ser Gly Leu Phe Thr Ile Glu Gly Phe Lys Glu  
 115 120 125  
 Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu Ala Val Leu Pro Ala Ala  
 130 135 140  
 Thr Thr Asn Asn Gly Ser Gln Thr Pro Thr Thr Ser Thr Pro Ser  
 145 150 155 160  
 Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu Asn Asn Glu  
 165 170 175  
 Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser Gly Asp Gly Gly Thr Ile  
 180 185 190  
 Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys Leu Cys Val Phe  
 195 200 205  
 Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys Gln Val Val Thr  
 210 215 220  
 Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala Phe Ile Ala Asn  
 225 230 235 240  
 Val Ala Gly Val Arg Gly Gly Gly Ile Ala Ala Val Gln Asp Gly Gln  
 245 250 255

Gln	Gly	Val	Ser	Ser	Ser	Thr	Ser	Thr	Glu	Asp	Pro	Val	Val	Ser	Phe	
			260					265					270			
Ser	Arg	Asn	Thr	Ala	Val	Glu	Phe	Asp	Gly	Asn	Val	Ala	Arg	Val	Gly	
		275					280					285				
Gly	Gly	Ile	Tyr	Ser	Tyr	Gly	Asn	Val	Ala	Phe	Leu	Asn	Asn	Gly	Lys	
	290					295					300					
Thr	Leu	Phe	Leu	Asn	Asn	Val	Ala	Ser	Pro	Val	Tyr	Ile	Ala	Ala	Glu	
305					310					315					320	
Gln	Pro	Thr	Asn	Gly	Gln	Ala	Ser	Asn	Thr	Ser	Asp	Asn	Tyr	Gly	Asp	
			325						330						335	
Gly	Gly	Ala	Ile	Phe	Cys	Lys	Asn	Gly	Ala	Gln	Ala	Ala	Gly	Ser	Asn	
		340						345					350			
Asn	Ser	Gly	Ser	Val	Ser	Phe	Asp	Gly	Glu	Gly	Val	Val	Phe	Phe	Ser	
		355					360					365				
Ser	Asn	Val	Ala	Ala	Gly	Lys	Gly	Gly	Ala	Ile	Tyr	Ala	Lys	Lys	Leu	
	370					375					380					
Ser	Val	Ala	Asn	Cys	Gly	Pro	Val	Gln	Phe	Leu	Gly	Asn	Ile	Ala	Asn	
385					390					395					400	
Asp	Gly	Gly	Ala	Ile	Tyr	Leu	Gly	Glu	Ser	Gly	Glu	Leu	Ser	Leu	Ser	
			405					410						415		
Ala	Asp	Tyr	Gly	Asp	Ile	Ile	Phe	Asp	Gly	Asn	Leu	Lys	Arg	Thr	Ala	
		420						425					430			
Lys	Glu	Asn	Ala	Ala	Asp	Val	Asn	Gly	Val	Thr	Val	Ser	Ser	Gln	Ala	
		435					440					445				
Ile	Ser	Met	Gly	Ser	Gly	Gly	Lys	Ile	Thr	Thr	Leu	Arg	Ala	Lys	Ala	
	450				455						460					
Gly	His	Gln	Ile	Leu	Phe	Asn	Asp	Pro	Ile	Glu	Met	Ala	Asn	Gly	Asn	
465				470						475					480	
Asn	Gln	Pro	Ala	Gln	Ser	Ser	Glu	Pro	Leu	Lys	Ile	Asn	Asp	Gly	Glu	
			485						490					495		
Gly	Tyr	Thr	Gly	Asp	Ile	Val	Phe	Ala	Asn	Gly	Asn	Ser	Thr	Leu	Tyr	
		500						505					510			
Gln	Asn	Val	Thr	Ile	Glu	Gln	Gly	Arg	Ile	Val	Leu	Arg	Glu	Lys	Ala	
	515						520					525				
Lys	Leu	Ser	Val	Asn	Ser	Leu	Ser	Gln	Thr	Gly	Gly	Ser	Leu	Tyr	Met	
	530				535						540					
Glu	Ala	Gly	Ser	Thr	Leu	Asp	Phe	Val	Thr	Pro	Gln	Pro	Pro	Gln	Gln	
545					550					555					560	
Pro	Pro	Ala	Ala	Asn	Gln	Leu	Ile	Thr	Leu	Ser	Asn	Leu	His	Leu	Ser	
			565						570					575		
Leu	Ser	Ser	Leu	Leu	Ala	Asn	Asn	Ala	Val	Thr	Asn	Pro	Pro	Thr	Asn	
		580						585					590			
Pro	Pro	Ala	Gln	Asp	Ser	His	Pro	Ala	Val	Ile	Gly	Ser	Thr	Thr	Ala	
		595					600					605				
Gly	Pro	Val	Thr	Ile	Ser	Gly	Pro	Phe	Phe	Phe	Glu	Asp	Leu	Asp	Asp	
	610					615					620					
Thr	Ala	Tyr	Asp	Arg	Tyr	Asp	Trp	Leu	Gly	Ser	Asn	Gln	Lys	Ile	Asp	
625					630					635					640	
Val	Leu	Lys	Leu	Gln	Leu	Gly	Thr	Gln	Pro	Ser	Ala	Asn	Ala	Pro	Ser	
			645						650					655		
Asp	Leu	Thr	Leu	Gly	Asn	Glu	Met	Pro	Lys	Tyr	Gly	Tyr	Gln	Gly	Ser	
		660						665					670			
Trp	Lys	Leu	Ala	Trp	Asp	Pro	Asn	Thr	Ala	Asn	Asn	Gly	Pro	Tyr	Thr	
		675					680					685				
Leu	Lys	Ala	Thr	Trp	Thr	Lys	Thr	Gly	Tyr	Asn	Pro	Gly	Pro	Glu	Arg	
	690					695					700					
Val	Ala	Ser	Leu	Val	Pro	Asn	Ser	Leu	Trp	Gly	Ser	Ile	Leu	Asp	Ile	
705					710					715					720	
Arg	Ser	Ala	His	Ser	Ala	Ile	Gln	Ala	Ser	Val	Asp	Gly	Arg	Ser	Tyr	
			725						730					735		
Cys	Arg	Gly	Leu	Trp	Val	Ser	Gly	Val	Ser	Asn	Phe	Ser	Tyr	His	Asp	
			740					745					750			

Arg Asp Ala Leu Gly Gln Gly Tyr Arg Tyr Ile Ser Gly Gly Tyr Ser  
 755 760 765  
 Leu Gly Ala Asn Ser Tyr Phe Gly Ser Ser Met Phe Gly Leu Ala Phe  
 770 775 780  
 Thr Glu Val Phe Gly Arg Ser Lys Asp Tyr Val Val Cys Arg Ser Asn  
 785 790 795 800  
 His His Ala Cys Ile Gly Ser Val Tyr Leu Ser Thr Lys Gln Ala Leu  
 805 810 815  
 Cys Gly Ser Tyr Leu Phe Gly Asp Ala Phe Ile Arg Ala Ser Tyr Gly  
 820 825 830  
 Phe Gly Asn Gln His Met Lys Thr Ser Tyr Thr Phe Ala Glu Glu Ser  
 835 840 845  
 Asp Val Arg Trp Asp Asn Asn Cys Leu Val Gly Glu Ile Gly Val Gly  
 850 855 860  
 Leu Pro Ile Val Thr Thr Pro Ser Lys Leu Tyr Leu Asn Glu Leu Arg  
 865 870 875 880  
 Pro Phe Val Gln Ala Glu Phe Ser Tyr Ala Asp His Glu Ser Phe Thr  
 885 890 895  
 Glu Glu Gly Asp Gln Ala Arg Ala Phe Arg Ser Gly His Leu Met Asn  
 900 905 910  
 Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg Cys Ser Ser Thr His  
 915 920 925  
 Pro Asn Lys Tyr Ser Phe Met Gly Ala Tyr Ile Cys Asp Ala Tyr Arg  
 930 935 940  
 Thr Ile Ser Gly Thr Gln Thr Thr Leu Leu Ser His Gln Glu Thr Trp  
 945 950 955 960  
 Thr Thr Asp Ala Phe His Leu Ala Arg His Gly Val Ile Val Arg Gly  
 965 970 975  
 Ser Met Tyr Ala Ser Leu Thr Ser Asn Ile Glu Val Tyr Gly His Gly  
 980 985 990  
 Arg Tyr Glu Tyr Arg Asp Thr Ser Arg Gly Tyr Gly Leu Ser Ala Gly  
 995 1000 1005  
 Ser Lys Val Arg Phe  
 1010

<210> 17  
 <211> 505  
 <212> PRT  
 <213> Chlamydia sp.

<400> 17  
 Glu Ile Met Val Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu Thr Val  
 1 5 10 15  
 Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe  
 20 25 30  
 Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala  
 35 40 45  
 Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu  
 50 55 60  
 Gly Arg Gly His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn  
 65 70 75 80  
 Gly Ala Ala Leu Ser Asn Ser Ala Ala Asp Gly Leu Phe Thr Ile Glu  
 85 90 95  
 Gly Phe Lys Glu Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu Ala Val  
 100 105 110  
 Leu Pro Ala Ala Thr Thr Asn Lys Gly Ser Gln Thr Pro Thr Thr Thr  
 115 120 125  
 Ser Thr Pro Ser Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu  
 130 135 140  
 Leu Asn Asn Glu Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser Gly Asp  
 145 150 155 160

Gly Gly Ala Ile Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys  
 165 170 175  
 Leu Cys Val Phe Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys  
 180 185 190  
 Gln Val Val Thr Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala  
 195 200 205  
 Phe Val Ala Asn Val Ala Gly Val Arg Gly Gly Gly Ile Ala Ala Val  
 210 215 220  
 Gln Asp Gly Gln Gln Gly Val Ser Ser Ser Thr Ser Thr Glu Asp Pro  
 225 230 235 240  
 Val Val Ser Phe Ser Arg Asn Thr Ala Val Glu Phe Asp Gly Asn Val  
 245 250 255  
 Ala Arg Val Gly Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu  
 260 265 270  
 Asn Asn Gly Lys Thr Leu Phe Leu Asn Asn Val Ala Ser Pro Val Tyr  
 275 280 285  
 Ile Ala Ala Lys Gln Pro Thr Ser Gly Gln Ala Ser Asn Thr Ser Asn  
 290 295 300  
 Asn Tyr Gly Asp Gly Gly Ala Ile Phe Cys Lys Asn Gly Ala Gln Ala  
 305 310 315 320  
 Gly Ser Asn Asn Ser Gly Ser Val Ser Phe Asp Gly Glu Gly Val Val  
 325 330 335  
 Phe Phe Ser Ser Asn Val Ala Ala Gly Lys Gly Gly Ala Ile Tyr Ala  
 340 345 350  
 Lys Lys Leu Ser Val Ala Asn Cys Gly Pro Val Gln Phe Leu Arg Asn  
 355 360 365  
 Ile Ala Asn Asp Gly Gly Ala Ile Tyr Leu Gly Glu Ser Gly Glu Leu  
 370 375 380  
 Ser Leu Ser Ala Asp Tyr Gly Asp Ile Ile Phe Asp Gly Asn Leu Lys  
 385 390 395 400  
 Arg Thr Ala Lys Glu Asn Ala Ala Asp Val Asn Gly Val Thr Val Ser  
 405 410 415  
 Ser Gln Ala Ile Ser Met Gly Ser Gly Gly Lys Ile Thr Thr Leu Arg  
 420 425 430  
 Ala Lys Ala Gly His Gln Ile Leu Phe Asn Asp Pro Ile Glu Met Ala  
 435 440 445  
 Asn Gly Asn Asn Gln Pro Ala Gln Ser Ser Lys Leu Leu Lys Ile Asn  
 450 455 460  
 Asp Gly Glu Gly Tyr Thr Gly Asp Ile Val Phe Ala Asn Gly Ser Ser  
 465 470 475 480  
 Thr Leu Tyr Gln Asn Val Thr Ile Glu Gln Gly Arg Ile Val Leu Arg  
 485 490 495  
 Glu Lys Ala Lys Leu Ser Val Asn Ser  
 500 505

<210> 18  
 <211> 57  
 <212> DNA  
 <213> Chlamydia sp.

<400> 18  
 aagggcccaa ttacgcagag ctcgagagaa attatgggttc ctcaaggaat ttacgat

57

<210> 19  
 <211> 20  
 <212> DNA  
 <213> Chlamydia sp.

<400> 19  
 cgctctagaa ctagtgatc

20

<210> 20

<211> 22  
 <212> DNA  
 <213> Chlamydia sp.

<400> 20  
 atggttcctc aaggaattta cg

22

<210> 21  
 <211> 19  
 <212> DNA  
 <213> Chlamydia sp.

<400> 21  
 ggtcccccat cagcgggag

19

<210> 22  
 <211> 1515  
 <212> DNA  
 <213> Chlamydia sp.

<400> 22  
 gaaatcatgg ttcctcaagg aatttacgat ggggagacgt taactgtatc atttccctat 60  
 actggttatag gagatccgag tgggactact gttttttctg caggagagtt aacattaaaa 120  
 aatcttgaca attctattgc agctttgcoo ttaagttggt ttgggaactt attagggagt 180  
 tttactgttt tagggagagg acactcgttg actttcgaga acatacggac ttctacaaat 240  
 ggggcagctc taagtaatag cgctgctgat ggactgttta ctattgaggg ttttaaagaa 300  
 ttatcctttt ccaattgcaa ttcattactt gccgtactgc ctgctgcaac gactaataag 360  
 ggtagccaga ctccgacgac aacatctaca ccgtctaatt gtactattta ttctaaaaa 420  
 gatctttttg tactcaataa tgagaagttc tcattctata gtaatttagt ctctggagat 480  
 gggggagcta tagatgctaa gagcttaacg gttcaaggaa ttagcaagct ttgtgtcttc 540  
 caagaaaata ctgctcaagc tgatggggga gcttgtcaag tagtcaccag tttctctgct 600  
 atggctaacg aggtccttat tgcctttgta gcgaatgttg caggagtaag agggggaggg 660  
 attgctgctg ttcaggatgg gcagcaggga gtgtcatcat ctacttcaac agaagatcca 720  
 gtagtaagtt tttccagaaa tactgcggta gagtttgatg ggaacgtagc ccgagtagga 780  
 ggaggggattt actcctacgg gaacgttgct ttcctgaata atggaaaaaac cttgtttctc 840  
 aacaatgttg cttctcctgt ttacattgct gctaagcaac caacaagtgg acaggcttct 900  
 aatacgagta ataattacgg agatggagga gctatcttct gtaagaatgg tgcgcaagca 960  
 ggatccaata actctggatc agtttccctt gatggagagg gagtagtttt ctttagtagc 1020  
 aatgtagctg ctgggaaagg gggagctatt tatgccaaaa agctctcggg tgctaactgt 1080  
 ggccctgtac aatttttaag gaatatcgct aatgatggtg gagcgattta tttaggagaa 1140  
 tctggagagc tcagttttatc tgctgattat ggagatatta ttttcgatgg gaatcttaaa 1200  
 agaacagcca aagagaatgc tgccgatgtt aatggcgtaa ctgtgtcctc acaagccatt 1260  
 tcgatgggat cgggagggaa aataacgaca ttaagagcta aagcagggca tcagattctc 1320  
 tttaatgata ccacgcagat ggcaaacgga aataaccagc cagcgcagtc ttccaaactt 1380  
 ctaaaaatta acgatggtga aggatacaca ggggatattg tttttgctaa tggaagcagt 1440  
 actttgtacc aaaatgttac gatagagcaa ggaaggattg ttcttcgtga aaaggcaaaa 1500  
 ttatcagtga attct 1515

<210> 23  
 <211> 3354  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Recombinant Expression Vector

<400> 23  
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 ttaactgtat catttcccta tactgttata ggagatccga gtgggactac tgttttttct 180  
 gcaggagagt taacgttaaa aaatcttgac aattctattg cagctttgcc ttttaagttg 240  
 tttgggaact tattagggag ttttactggt ttagggagag gacactcgtt gactttcgag 300



aacatacggg	cttctacaaa	tggagctgca	ctaagtgaca	gcgctaatag	cgggttattt	360
actattgagg	gttttaaaaga	attatctttt	tccaattgca	acccattact	tgccgtactg	420
cctgctgcaa	cgactaataa	tggtagccag	actccgctga	caacatctac	accgtctaatt	480
ggtactattt	attctaaaaa	agatcttttg	ttactcaata	atgagaagtt	ctcatttctat	540
agtaattcag	tctctggaga	tgggggagct	atagatgcta	agagcttaac	ggttcaaggga	600
attagcaagc	tttgtgtott	ccaagaaaat	actgctcaag	ctgatggggg	agcttgtcaa	660
gtagtcacca	gtttctctgc	tatggctaac	gaggctccta	ttgcctttgt	agcgaatggt	720
gcaggagtaa	gagggggagg	gattgctgct	gttcaggatg	ggcagcaggg	agtgtcatca	780
tctacttcaa	cagaagatcc	agtagtaagt	ttttccagaa	atactgcggt	agagtttgat	840
gggaacgtag	cccagtagtg	aggagggatt	tactcctacg	ggaacgttgc	tttctctgaat	900
aatggaaaaa	ccttgtttct	caacaatggt	gcttctcctg	tttacattgc	tgctgagcaa	960
ccaacaaatg	gacaggcttc	taatacagag	gataattacg	gagatggagg	agctatcttc	1020
tgtaagaatg	gtgcgcaagc	agcaggatcc	aataactctg	gatcagtttc	ctttgatgga	1080
gagggagtag	ttttcttttag	tagcaatgta	gctgctggga	aagggggagc	tatttatgcc	1140
aaaaagctct	cgggttgctaa	ctgtggccct	gtacaactct	tagggaatat	cgctaattgat	1200
ggtggagcga	tttattttagg	agaatctgga	gagctcagtt	tatctgctga	ttatggagat	1260
atgattttctg	atgggaatct	taaaagaaca	gccaaagaga	atgctgccga	tgттаatggc	1320
gtaactgtgt	cctcacaagc	catttcgatg	ggatcgggag	ggaaaataac	gacattaaga	1380
gctaaagcag	ggcatcagat	tctctttaat	gatcccatcg	agatggcaaa	cggaaataac	1440
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ctgaaattac	agttagggac	tcagcccca	gctaattgcc	catcagattt	gactctaggg	1980
aatgagatgc	ctaagtatgg	ctatcaagga	agctggaagc	ttgcgtggga	tcctaataca	2040
gcaataatg	gtccttatac	tctgaaagct	acatggacta	aaactgggta	taatcctggg	2100
cctgagcgag	tgccttcttt	ggttccaaat	agtttatggg	gatccatttt	agataacga	2160
tctgcgcatt	cagcaattca	agcaagtgtg	gatgggcgct	cttattgtcg	aggattatgg	2220
gtttctggag	tttcgaattt	cttctatcat	gaccgcgatg	ctttaggtca	gggatatcgg	2280
tatattagtg	ggggttattc	cttaggagca	aactcctact	ttggatcatc	gatgttttgt	2340
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catgcttgca	taggatccgt	ttatctatct	accaaacagg	ctttatgtgg	atccttatgtg	2460
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gcttatcgca	ccatctctgg	gactcagaca	acactcctat	cccatcaaga	gacatggaca	2880
acagatgcct	ttcatttggc	aagacattga	gtcatagtta	gaggggtctat	gtatgcttct	2940
ctaacaagca	atatagaagt	atatggccat	ggaagatag	agtatcgaga	tacttctcga	3000
ggttatgggt	tgagtgcagg	aagtaaagtc	cggttctaaa	aatattgggt	agatagttaa	3060
gtgttagcga	tgcccttttc	tttgagatct	acatcatttt	gttttttagc	ttgtttgtgt	3120
tcctattcgt	atggattcgc	gagctctcct	caagtgttaa	cacctaatgt	aacctactct	3180
tttaaggggg	acgatgttta	cttgaatgga	gactgcgctt	ttgtcaatgt	ctatgcaggg	3240
gcagagaacg	gctcaattat	ctcagctaag	ggcgacaatt	taacgattac	cggacaaaac	3300
catacattat	cattttacaca	ttctcaaggg	ccagttcttc	aaaattagcc	ttca	3354

<210> 24

<211> 3324

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant Expression Vector

<400> 24

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ttaagtgggg gggggtatgc agcagaaatc atgattcctc aaggaattta cgatggggag 120

acgttaactg	tatcattttcc	ctatactggt	ataggagatc	cgagtgggac	tactgttttt	180
tctgcaggag	agttaacggt	aaaaaatctt	gacaattcta	ttgcagcttt	gcctttaagt	240
tgttttggga	acttattagg	gagttttact	gttttaggga	gaggacactc	gttgactttc	300
gagaacatac	ggacttctac	aaatggagct	gcactaagt	acagcgctaa	tagcgggtta	360
tttactattg	agggttttta	agaattatct	ttttccaatt	gcaactcatt	acttgccgta	420
ctgcoctgctg	caacgactaa	taatggtagc	cagactccga	cgacaacatc	tacaccgtct	480
aatgggtacta	tttatttcta	aacagatctt	ttgttactca	ataatgagaa	gttctcattc	540
tatagtaatt	tagtctctgg	agatggggga	actatagatg	ctaagagctt	aacggttcaa	600
ggaattagca	agctttgtgt	cttccaagaa	aatactgctc	aagctgatgg	gggagcttgt	660
caagtagtca	ccagtttctc	tgctatggct	aacgaggctc	ctattgcctt	tatagcgaat	720
gttgacaggag	taagaggggg	agggattgct	gctgttcagg	atgggcagca	gggagtgtca	780
tcacttactt	caacagaaga	tccagtagta	agtttttcca	gaaatactgc	ggtagagttt	840
gatgggaacg	tagcccgagt	aggaggagg	atttactcct	acgggaacgt	tgctttcctg	900
aataatggaa	aaaccttggt	tctcaacaat	ctgtttcttc	ctgtttacat	tgctgctgag	960
caaccaacaa	atggacaggc	ttctaatacg	agtataatt	acggagatgg	aggagctatc	1020
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gatgggtggag	cgattttatt	aggagaatct	ggagagctca	gtttatctgc	tgattatgga	1260
gatatttatt	tcgatgggaa	tcttaaaaga	acagccaaag	agaatgctgc	cgatgttaat	1320
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gatattgttt	ttgctaattg	aaacagtaact	ttgtaccaa	atgttacgat	agagcaagga	1560
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gcagtcattg	gtagcacaac	tgctgggtcct	gtcacaatta	gtgggccttt	cttttttgag	1860
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gggcctgagc	gagtagcttc	tttgggtcca	aatagtttat	ggggatccat	tttagatata	2160
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cggtatatta	gtgggggtta	ttccttagga	gcaaactcct	actttggatc	atcgatgttt	2340
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caagctcggg	cattcaggag	tggatcatctc	atgaatctat	cagttcctgt	tggagtaaaa	2760
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gatgcttata	gcaccatctc	tgggactcag	acaacactcc	tatcccatca	agagacatgg	2880
acaacagatg	cctttcattt	ggcaagacat	ggagtcatag	ttagagggtc	tatgtatgct	2940
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ccttttaagg	gggacgatgt	ttacttgaat	ggagactgcg	cttttagtcaa	tgtctatgca	3240
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aaccatgcat	tatcattttac	agat				3324

<210> 25  
 <211> 65  
 <212> PRT  
 <213> Chlamydia sp.

<400> 25  
 Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe Ser Ala  
 1 5 10 15  
 Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala Pro Leu  
 20 25 30  
 Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu Gly Arg Gly  
 35 40 45  
 His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn Gly Ala Ala  
 50 55 60  
 Leu

65

<210> 26  
 <211> 24  
 <212> PRT  
 <213> Chlamydia sp.

<400> 26  
 Ala Ala Asn Gln Leu Ile Thr Leu Ser Asn Leu His Leu Ser Leu Ser  
 1 5 10 15  
 Ser Leu Leu Ala Asn Asn Ala Val  
 20

<210> 27  
 <211> 8  
 <212> PRT  
 <213> Chlamydia sp.

<400> 27  
 Gly Tyr Thr Gly Asp Ile Val Phe  
 1 5  
 <210> 28  
 <211> 7  
 <212> PRT  
 <213> Chlamydia sp.

<400> 28  
 Tyr Gly Asp Ile Ile Phe Asp  
 1 5  
 <210> 29  
 <211> 63  
 <212> PRT  
 <213> Chlamydia sp.

<400> 29  
 Gly Tyr Ala Ala Glu Ile Met Val Pro Gln Gly Ile Tyr Asp Gly Glu  
 1 5 10 15  
 Thr Leu Thr Val Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly  
 20 25 30  
 Thr Thr Val Phe Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn  
 35 40 45  
 Ser Ile Ala Ala Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu Gly  
 50 55 60

<210> 30  
 <211> 22  
 <212> PRT  
 <213> Chlamydia sp.

<400> 30  
 Met Ala Asn Gly Asn Asn Gln Pro Ala Gln Ser Ser Lys Leu Leu Lys  
 1 5 10 15  
 Ile Asn Asp Gly Glu Gly  
 20

<210> 31

<211> 14  
<212> PRT  
<213> Chlamydia sp.

<400> 31  
Ala Asn Gly Ser Ser Thr Leu Tyr Gln Asn Val Thr Ile Glu  
1 5 10  
<210> 32  
<211> 10  
<212> PRT  
<213> Chlamydia sp.

<400> 32  
Lys Leu Ser Val Asn Ser Leu Ser Gln Thr  
1 5 10  
<210> 33  
<211> 45  
<212> PRT  
<213> Chlamydia sp.

<400> 33  
Val Ile Gly Ser Thr Thr Ala Gly Ser Val Thr Ile Ser Gly Pro Ile  
1 5 10 15  
Phe Phe Glu Asp Leu Asp Asp Thr Ala Tyr Asp Arg Tyr Asp Trp Leu  
20 25 30  
Gly Ser Asn Gln Lys Ile Asn Val Leu Lys Leu Gln Leu  
35 40 45  
<210> 34  
<211> 64  
<212> PRT  
<213> Chlamydia sp.

<400> 34  
Val Ile Gly Ser Thr Thr Ala Gly Ser Val Thr Ile Ser Gly Pro Ile  
1 5 10 15  
Phe Phe Glu Asp Leu Asp Asp Thr Ala Tyr Asp Arg Tyr Asp Trp Leu  
20 25 30  
Gly Ser Asn Gln Lys Ile Asn Val Leu Lys Leu Gln Leu Gly Thr Lys  
35 40 45  
Pro Pro Ala Asn Ala Pro Ser Asp Leu Thr Leu Gly Asn Glu Met Pro  
50 55 60  
<210> 35  
<211> 10  
<212> PRT  
<213> Chlamydia sp.

<400> 35  
Asp Pro Asn Thr Ala Asn Asn Gly Pro Tyr  
1 5 10  
<210> 36  
<211> 458  
<212> PRT  
<213> Chlamydia sp.

<400> 36  
Gly Gly Ala Cys Gln Val Val Thr Ser Phe Ser Ala Met Ala Asn Glu  
1 5 10 15  
Ala Pro Ile Ala Phe Val Ala Asn Val Ala Gly Val Arg Gly Gly Gly  
20 25 30  
Ile Ala Ala Val Gln Asp Gly Gln Gln Gly Val Ser Ser Ser Thr Ser  
35 40 45  
Thr Glu Asp Pro Val Val Ser Phe Ser Arg Asn Thr Ala Val Glu Phe

50	55	60
Asp Gly Asn Val Ala Arg Val Gly Gly Gly Ile Tyr Ser Tyr Gly Asn		
65	70	75
Val Ala Phe Leu Asn Asn Gly Lys Thr Leu Phe Leu Asn Asn Val Ala		
	85	90
Ser Pro Val Tyr Ile Ala Ala Lys Gln Pro Thr Ser Gly Gln Ala Ser		
	100	105
Asn Thr Ser Asn Asn Tyr Gly Asp Gly Gly Ala Ile Phe Cys Lys Asn		
	115	120
Gly Ala Gln Ala Gly Ser Asn Asn Ser Gly Ser Val Ser Phe Asp Gly		
	130	135
Glu Gly Val Val Phe Phe Ser Ser Asn Val Ala Ala Gly Lys Gly Gly		
145	150	155
Ala Ile Tyr Ala Lys Lys Leu Ser Val Ala Asn Cys Gly Pro Val Gln		
	165	170
Phe Leu Arg Asn Ile Ala Asn Asp Gly Gly Ala Ile Tyr Leu Gly Glu		
	180	185
Ser Gly Glu Leu Ser Leu Ser Ala Asp Tyr Gly Asp Ile Ile Phe Asp		
	195	200
Gly Asn Leu Lys Arg Thr Ala Lys Glu Asn Ala Ala Asp Val Asn Gly		
	210	215
Val Thr Val Ser Ser Gln Ala Ile Ser Met Gly Ser Gly Gly Lys Ile		
225	230	235
Thr Thr Leu Arg Ala Lys Ala Gly His Gln Ile Leu Phe Asn Asp Pro		
	245	250
Ile Glu Met Ala Asn Gly Asn Asn Gln Pro Ala Gln Ser Ser Lys Leu		
	260	265
Leu Lys Ile Asn Asp Gly Glu Gly Tyr Thr Gly Asp Ile Val Phe Ala		
	275	280
Asn Gly Ser Ser Thr Leu Tyr Gln Asn Val Thr Ile Glu Gln Gly Arg		
	290	295
Ile Val Leu Arg Glu Lys Ala Lys Leu Ser Val Asn Ser Leu Ser Gln		
305	310	315
Thr Gly Gly Ser Leu Tyr Met Glu Ala Gly Ser Thr Trp Asp Phe Val		
	325	330
Thr Pro Gln Pro Pro Gln Gln Pro Pro Ala Ala Asn Gln Leu Ile Thr		
	340	345
Leu Ser Asn Leu His Leu Ser Leu Ser Ser Leu Leu Ala Asn Asn Ala		
	355	360
Val Thr Asn Pro Pro Thr Asn Pro Pro Ala Gln Asp Ser His Pro Ala		
	370	375
Val Ile Gly Ser Thr Thr Ala Gly Ser Val Thr Ile Ser Gly Pro Ile		
385	390	395
Phe Phe Glu Asp Leu Asp Asp Thr Ala Tyr Asp Arg Tyr Asp Trp Leu		
	405	410
Gly Ser Asn Gln Lys Ile Asn Val Leu Lys Leu Gln Leu Gly Thr Lys		
	420	425
Pro Pro Ala Asn Ala Pro Ser Asp Leu Thr Leu Gly Asn Glu Met Pro		
	435	440
Lys Tyr Gly Tyr Gln Gly Ser Trp Lys Leu		
	450	455

<210> 37  
 <211> 325  
 <212> PRT  
 <213> Chlamydia sp.

<400> 37  
 Leu Lys Ala Thr Trp Thr Lys Thr Gly Tyr Asn Pro Gly Pro Glu Arg  
 1 5 10 15  
 Val Ala Ser Leu Val Pro Asn Ser Leu Trp Gly Ser Ile Leu Asp Ile  
 20 25 30  
 Arg Ser Ala His Ser Ala Ile Gln Ala Ser Val Asp Gly Arg Ser Tyr



<212> DNA  
 <213> Chlamydia sp.

<400> 41  
 000  
 <210> 42  
 <211> 6  
 <212> PRT  
 <213> Chlamydia sp.

<400> 42  
 Glu Ile Met Val Pro Gln  
 1 5  
 <210> 43  
 <211> 984  
 <212> PRT  
 <213> Chlamydia sp.

<400> 43  
 Glu Ile Met Val Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu Thr Val  
 1 5 10 15  
 Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe  
 20 25 30  
 Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala  
 35 40 45  
 Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu  
 50 55 60  
 Gly Arg Gly His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn  
 65 70 75 80  
 Gly Ala Ala Leu Ser Asn Ser Ala Ala Asp Gly Leu Phe Thr Ile Glu  
 85 90 95  
 Gly Phe Lys Glu Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu Ala Val  
 100 105 110  
 Leu Pro Ala Ala Thr Thr Asn Lys Gly Ser Gln Thr Pro Thr Thr Thr  
 115 120 125  
 Ser Thr Pro Ser Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu  
 130 135 140  
 Leu Asn Asn Glu Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser Gly Asp  
 145 150 155 160  
 Gly Gly Ala Ile Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys  
 165 170 175  
 Leu Cys Val Phe Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys  
 180 185 190  
 Gln Val Val Thr Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala  
 195 200 205  
 Phe Val Ala Asn Val Ala Gly Val Arg Gly Gly Gly Ile Ala Ala Val  
 210 215 220  
 Gln Asp Gly Gln Gln Gly Val Ser Ser Ser Thr Ser Thr Glu Asp Pro  
 225 230 235 240  
 Val Val Ser Phe Ser Arg Asn Thr Ala Val Glu Phe Asp Gly Asn Val  
 245 250 255  
 Ala Arg Val Gly Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu  
 260 265 270  
 Asn Asn Gly Lys Thr Leu Phe Leu Asn Asn Val Ala Ser Pro Val Tyr  
 275 280 285  
 Ile Ala Ala Lys Gln Pro Thr Ser Gly Gln Ala Ser Asn Thr Ser Asn  
 290 295 300  
 Asn Tyr Gly Asp Gly Gly Ala Ile Phe Cys Lys Asn Gly Ala Gln Ala  
 305 310 315 320  
 Gly Ser Asn Asn Ser Gly Ser Val Ser Phe Asp Gly Glu Gly Val Val  
 325 330 335  
 Phe Phe Ser Ser Asn Val Ala Ala Gly Lys Gly Gly Ala Ile Tyr Ala





		835				840				845				
Glu	Leu	Arg	Pro	Phe	Val	Gln	Ala	Glu	Phe	Ser	Tyr	Ala	Asp	His
	850					855					860			
Ser	Phe	Thr	Glu	Glu	Gly	Asp	Gln	Ala	Arg	Ala	Phe	Lys	Ser	Gly
865					870					875				880
Leu	Leu	Asn	Leu	Ser	Val	Pro	Val	Gly	Val	Lys	Phe	Asp	Arg	Cys
				885					890					895
Ser	Thr	His	Pro	Asn	Lys	Tyr	Ser	Phe	Met	Ala	Ala	Tyr	Ile	Cys
			900					905					910	Asp
Ala	Tyr	Arg	Thr	Ile	Ser	Gly	Thr	Glu	Thr	Thr	Leu	Leu	Ser	His
			915					920					925	Gln
Glu	Thr	Trp	Thr	Thr	Asp	Ala	Phe	His	Leu	Ala	Arg	His	Gly	Val
	930					935					940			Val
Val	Arg	Gly	Ser	Met	Tyr	Ala	Ser	Leu	Thr	Ser	Asn	Ile	Glu	Val
945					950					955				Tyr
Gly	His	Gly	Arg	Tyr	Glu	Tyr	Arg	Asp	Ala	Ser	Arg	Gly	Tyr	Gly
				965					970					Leu
Ser	Ala	Gly	Ser	Arg	Val	Arg	Phe							975
			980											